

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WASTFALT, Maria K. Boden
FLOCK, Jan-Ingmar
- (ii) TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
(B) STREET: P.O. Box 1404
(C) CITY: Alexandria
(D) STATE: Virginia
(E) COUNTRY: United States
(F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TBA (Div of US 09/276,141)
(B) FILING DATE: Even date herewith
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/276,141
(B) FILING DATE: 25-03-99
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/244,229
(B) FILING DATE: 09-DEC-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: SE 9202720-0
(B) FILING DATE: 21-SEP-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: SE 9302955-1
(B) FILING DATE: 13-SEP-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/SE93/00759
(B) FILING DATE: 20-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: McGowan, Malcolm K.

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(B) REGISTRATION NUMBER: 39,300
(C) REFERENCE/DOCKET NUMBER: 012889-011

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (703) 836-6620
(B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Asn Ser
1 5 10 15

Lys Tyr Gly Thr
 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Lys Ser
1 5 10 15

Lys Lys Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
1 5 10 15
Lys Asn Gly Thr
20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
1 5 10 15
Lys Asn Gly Thr
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
1 5 10 15
Asn Ile Val Glu
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Tyr Pro Glu Lys Lys Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|--|-----|
| GAGCGAAGGA TACGGTCCAA GAGAAAAGAA ACCAGTGAGT ATTAATCACA ATATCGTAGA | 60 |
| GTACAATGAT GGTACTTTTA AATATCAATC TAGACCAAAA TTAACTCAA CACCTAAATA | 120 |
| TATTAAATTC AAACATGACT ATAATATTTT AGAATTTAAC GATGGTACAT TCGAATATGG | 180 |
| TGCACGTCCA CAATTTAATA AACCAGCAGC GAAAACGTGAT GCAACTATTA AAAAAGAACA | 240 |
| AAAATTGATT CAAGCTCAAA ATCTTGTGAG AGAATTTGAA AAAACACATA CTGTCAGTGC | 300 |
| ACACAGAAAA GCACAAAAGG CAGTCAACTT AGTTTCGTTT GAATACAAAG TGAAGAAAAT | 360 |
| GGTCTTACAA GAGCGAATTG ATAATGTATT AAAACAAGGA TTAGTGAG | 408 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | |
|---|--|
| Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His | |
| 1 5 10 15 | |
| Asn Ile Val Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro | |
| 20 25 30 | |
| Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn | |
| 35 40 45 | |

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Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln
50 55 60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln
65 70 75 80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His
85 90 95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser
100 105 110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn
115 120 125

Val Leu Lys Gln Gly Leu Val Arg
130 135

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 157..654

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 804..1007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTAGTGTA TAAGTGCTGA TGAGTCACAA GATAGATAAC TATATTTTGT CTATATTATA 60

AAGTGTTTAT AGTTAATTAA TAATTAGTTA ATTTCAAAAG TTGTATAAAT AGGATAACTT 120

AATAAATGTA AGATAATAAT TTGGAGGATA ATTAAC ATG AAA AAT AAA TTG ATA 174
Met Lys Asn Lys Leu Ile
1 5

GCA AAA TCT TTA TTA ACA ATA GCG GCA ATT GGT ATT ACT ACA ACT ACA 222
Ala Lys Ser Leu Leu Thr Ile Ala Ala Ile Gly Ile Thr Thr Thr Thr
10 15 20

ATT GCG TCA ACA GCA GAT GCG AGC GAA GGA TAC GGT CCA AGA GAA AAG 270
Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro Arg Glu Lys
25 30 35

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| | |
|---|-----|
| AAA CCA GTG AGT ATT AAT CAC AAT ATC GTA GAG TAC AAT GAT GGT ACT | 318 |
| Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn Asp Gly Thr | |
| 40 45 50 | |
| TTT AAA TAT CAA TCT AGA CCA AAA TTT AAC TCA ACA CCT AAA TAT ATT | 366 |
| Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro Lys Tyr Ile | |
| 55 60 65 70 | |
| AAA TTC AAA CAT GAC TAT AAT ATT TTA GAA TTT AAC GAT GGT ACA TTC | 414 |
| Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp Gly Thr Phe | |
| 75 80 85 | |
| GAA TAT GGT GCA CGT CCA CAA TTT AAT AAA CCA GCA GCG AAA ACT GAT | 462 |
| Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala Lys Thr Asp | |
| 90 95 100 | |
| GCA ACT ATT AAA AAA GAA CAA AAA TTG ATT CAA GCT CAA AAT CTT GTG | 510 |
| Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln Asn Leu Val | |
| 105 110 115 | |
| AGA GAA TTT GAA AAA ACA CAT ACT GTC AGT GCA CAC AGA AAA GCA CAA | 558 |
| Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg Lys Ala Gln | |
| 120 125 130 | |
| AAG GCA GTC AAC TTA GTT TCG TTT GAA TAC AAA GTG AAG AAA ATG GTC | 606 |
| Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys Lys Met Val | |
| 135 140 145 150 | |
| TTA CAA GAG CGA ATT GAT AAT GTA TTA AAA CAA GGA TTA GTG AGA TAA | 654 |
| Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu Val Arg * | |
| 155 160 165 | |
| TACTTCTGTC ATTATTTTAA GTTCAAAATA ATTTAATATT ATATTATTTT TTATTAATAA | 714 |
| AACGACTATG CTATTTAATG CCAGGTTAAT GTAACCTTCC TAAAATTGAC TATATAATCG | 774 |
| TTAAGTATCA ATTTTAAGGA GAGTTTACA ATG AAA TTT AAA AAA TAT ATA TTA | 827 |
| Met Lys Phe Lys Lys Tyr Ile Leu | |
| 1 5 | |
| ACA GGA ACA TTA GCA TTA CTT TTA TCA TCA ACT GGG ATA GCA ACT ATA | 875 |
| Thr Gly Thr Leu Ala Leu Leu Ser Ser Thr Gly Ile Ala Thr Ile | |
| 10 15 20 | |
| GAA GGG AAT AAA GCA GAT GCA AGT AGT CTG GAC AAA TAT TTA ACT GAA | 923 |
| Glu Gly Asn Lys Ala Asp Ala Ser Ser Leu Asp Lys Tyr Leu Thr Glu | |
| 25 30 35 40 | |
| AGT CAG TTT CAT GAT AAA CGC ATA GCA GAA GAA TTA AGA ACT TTA CTT | 971 |
| Ser Gln Phe His Asp Lys Arg Ile Ala Glu Glu Leu Arg Thr Leu Leu | |
| 45 50 55 | |

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| | |
|--|------|
| AAC AAA TCG AAT GTA TAT GCA TTA GCT GCA GGA AGC TT | 1009 |
| Asn Lys Ser Asn Val Tyr Ala Leu Ala Ala Gly Ser | |
| 60 65 | |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | |
|--|-----|
| ATAGATAACT ATATTTTGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA | 60 |
| TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA | 120 |
| TTAACATGAA AAATAAATTG ATAGCAAAAT CTTTATTAAC AATAGCGGCA ATTGGTATTA | 180 |
| CTACAAC TAC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA | 240 |
| AACCAAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT | 300 |
| CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT | 360 |
| TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG | 420 |
| CGAAAAC TGA TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA | 480 |
| GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT | 540 |
| TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT | 600 |
| TAAACAAGG ATTAGTGAGA TAATACTTCT GTCATTATTT TAAGTTCAAA ATAATTTAAT | 660 |
| ATTATATTAT TTTTATTAA TAAAACGACT ATGCTATTTA ATGCCAGGTT AATGTAACTT | 720 |
| TCCTAAAATT GACTATATAA TCGTTAAGTA TCAATTTTAA GGAGAGTTTA CAATGAAATT | 780 |
| T | 781 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|-----|
| ATAGATAGCT ATATTCAGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA | 60 |
| TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA | 120 |
| TTGACATGAA AAATGCATTG ATAGCAAAAT CTTTATTAAC ATTAGCGGCA ATAGGTATTA | 180 |
| CTACAACTAC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA | 240 |
| AACCAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT | 300 |
| CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT | 360 |
| TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG | 420 |
| CGAAAACTGA TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA | 480 |
| GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT | 540 |
| TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT | 600 |
| TAAAACAAGG ATTAGTTAAA TAAAACTTCA ATCGTTGCTG TTATCTGGAA ATAATTAATT | 660 |
| AAATGTTATG TTAATTTTTG TTAATGAAAA AAGTAATCTA TTTAATGACA GGTTAATGTA | 720 |
| ATTGTCCTGA AATTGACTAT ATACTCAGTA AGTATCAATT TTAAGGAGAG CTTATAATGA | 780 |
| AATT | 785 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Lys | Leu | Ile | Ala | Lys | Ser | Leu | Leu | Thr | Ile | Ala | Ala | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Ile | Thr | Thr | Thr | Thr | Ile | Ala | Ser | Thr | Ala | Asp | Ala | Ser | Glu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Gly | Pro | Arg | Glu | Lys | Lys | Pro | Val | Ser | Ile | Asn | His | Asn | Ile | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |

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(2) INFORMATION FOR SEQ ID NO:13:

(A) LENGTH: 165 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Ala | Leu | Ile | Ala | Lys | Ser | Leu | Leu | Thr | Leu | Ala | Ala | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Ile | Thr | Thr | Thr | Thr | Ile | Ala | Ser | Thr | Ala | Asp | Ala | Ser | Glu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Gly | Pro | Arg | Glu | Lys | Lys | Pro | Val | Ser | Ile | Asn | His | Asn | Ile | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Tyr | Asn | Asp | Gly | Thr | Phe | Lys | Tyr | Gln | Ser | Arg | Pro | Lys | Phe | Asn |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Thr | Pro | Lys | Tyr | Ile | Lys | Phe | Lys | His | Asp | Tyr | Asn | Ile | Leu | Glu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Phe | Asn | Asp | Gly | Thr | Phe | Glu | Tyr | Gly | Ala | Arg | Pro | Gln | Phe | Asn | Lys |
| | | | | 85 | | | | | 90 | | | | | 95 | |

Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile
 100 105 110

Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser
 115 120 125

Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr
 130 135 140

Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys
 145 150 155 160

Gln Gly Leu Val Lys
 165

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
 1 5 10 15

Asn Ile Val Glu Tyr Asn Asp Gly Ser Phe Lys Tyr Gln Ser Arg Pro
 20 25 30

Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn
 35 40 45

Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln
 50 55 60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln
 65 70 75 80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His
 85 90 95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser
 100 105 110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn
 115 120 125

Val Leu Lys Gln Gly Leu Val Arg
 130 135

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Gln | Tyr | Gly | Pro | Arg | Pro | Gln | Phe | Asn | Lys | Thr | Pro | Lys | Tyr | 1 | 5 | 10 | 15 |
| Val | Lys | Tyr | Arg | Asp | Ala | Gly | Thr | Gly | Ile | Arg | Glu | Tyr | Asn | Asp | Gly | 20 | 25 | 30 | |
| Thr | Phe | Gly | Tyr | Glu | Ala | Arg | Pro | Arg | Phe | Asn | Lys | Pro | Ser | Glu | Thr | 35 | 40 | 45 | |
| Asn | Ala | Tyr | Asn | Val | Thr | Thr | His | Ala | Asn | Gly | Gln | Val | Ser | Tyr | Gly | 50 | 55 | 60 | |
| Ala | Arg | Pro | Thr | Tyr | Lys | Lys | Pro | Ser | Glu | Thr | Asn | Ala | Tyr | Asn | Val | 65 | 70 | 75 | 80 |
| Thr | Thr | His | Ala | Asn | Gly | Gln | Val | Ser | Tyr | Gly | Ala | Arg | Pro | Thr | Gln | 85 | 90 | 95 | |
| Asn | Lys | Pro | Ser | Glu | Thr | Asn | Ala | Tyr | Asn | Val | Thr | Thr | His | Gly | Asn | 100 | 105 | 110 | |
| Gly | Gln | Val | Ser | Tyr | Gly | Ala | Arg | Gln | Ala | Gln | Asn | Lys | Pro | Ser | Lys | 115 | 120 | 125 | |
| Thr | Asn | Ala | Tyr | Asn | Val | Thr | Thr | His | Ala | Asn | Gly | Gln | Val | Ser | Tyr | 130 | 135 | 140 | |
| Gly | Ala | Arg | Pro | Thr | Tyr | Lys | Lys | Pro | Ser | Lys | Thr | Asn | Ala | Tyr | Asn | 145 | 150 | 155 | 160 |
| Val | Thr | Thr | His | Ala | Asp | Gly | Thr | Ala | Thr | Tyr | Gly | Pro | Arg | Val | Thr | 165 | 170 | 175 | |
| Lys | | | | | | | | | | | | | | | | | | | |

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